We claim:

1. A method to amplify an RNA molecule, comprising:

obtaining said RNA molecule;

introducing to said mRNA molecule a first primer, wherein said first primer comprises a region that hybridizes under suitable conditions to a complementary region of said RNA molecule;

introducing to said RNA molecule and said first primer a second primer, wherein said second primer comprises at least one riboguanine at the 3′ end of said primer;

synthesizing a first complementary nucleic acid molecule to said RNA molecule by extending said first primer using reverse transcriptase under conditions wherein said synthesis results in there being more than one cytosine at the 3′ end of said first complementary nucleic acid molecule, wherein said synthesis results in an RNA-first complementary nucleic acid molecule hybrid comprising the first primer and its extension product bound to the second primer and the RNA;

removing said RNA molecule and said second primer from said hybrid;

synthesizing a second complementary nucleic acid molecule to said first complementary nucleic acid molecule, wherein said synthesis results in a first complementary nucleic acid molecule and second complementary nucleic acid molecule hybrid, wherein the hybrid further comprises both a third primer with a sequence substantially similar to the second primer and an extension product of the third primer bound to the first complementary nucleic acid molecule; and

transcribing at least one mRNA molecule from said first complementary nucleic acid molecule and second complementary nucleic acid molecule hybrid.

2. The method of claim 1, wherein said RNA molecule is an mRNA molecule.

3. The method of claim 1, wherein said RNA is a tRNA molecule.

4. The method of claim 1, wherein said RNA is a rRNA molecule.

5. The method of claim 1, wherein said RNA molecule is obtained from a plurality of RNA molecules.

6. The method of claim 5, wherein said plurality of RNA molecules comprises mRNA, tRNA, rRNA, or a combination thereof.

7. The method of claim 1, wherein said first primer further comprises a region comprising at least two poly(dT)s.

8. The method of claim 1, wherein said first primer is a short primer of random sequence.

9. The method of claim 1, wherein said first primer further comprises a region selected from the group consisting of a promoter region, a restriction enzyme digestion sequence, and a combination thereof.

10. The method of claim 1, wherein said first primer further comprises a promoter region.

11. The method of claim 10, wherein said promoter is a bacteriophage transcription promoter.

12. The method of claim 11, wherein said bacteriophage transcription promoter is selected from the group consisting of T7 RNA polymerase promoter, T3 RNA polymerase promoter, SP6 RNA polymerase promoter, and a recombinant promoter.

13. The method of claim 1, wherein said second primer comprises a random sequence at it 5′ end and at least one guanine, deoxyguanine, cytosine, or deoxycytosine at its 3′ end.

14. The method of claim 1, wherein said second primer comprises a random sequence at it 5′ end and at least one guanine or cytosine at its 3′ end.

15. The method of claim 13, wherein said second primer further comprises a region selected from the group consisting of a promoter region, a protein translation start region, a restriction enzyme digestion sequence, and a combination thereof.

16. The method of claim 1, wherein said second primer further comprises a promoter.

17. The method of claim 16, wherein said promoter is a bacteriophage transcription promoter.

18. The method of claim 17, wherein said bacteriophage transcription promoter is selected from the group consisting of T7 RNA polymerase promoter, T3 RNA polymerase promoter, SP6 RNA polymerase promoter, and a recombinant promoter.

19. The method of claim 1, wherein said reverse transcriptase is selected from the group consisting of *Taq* reverse transcriptase, Moloney Murine Leukemia Virus reverse transcriptase, Moloney Murine Leukemia Virus reverse transcriptase lacking RNAseH activity, Avian Myeloblastosis Virus reverse transcriptase, Avian Myeloblastosis Virus reverse transcriptase lacking RNAseH activity, human T-cell leukemia virus type I (HTLV-I), Rous-associated virus 2 (RAV2), bovine leukemia virus (BLV), Rous sarcoma virus (RSV), HIV-1 reverse transcriptase, TERT reverse transcriptase, and *Tth* reverse transcriptase.

20. The method of claim 1, wherein said method further comprises at least one step of reverse transcribing said mRNA molecule from said transcription step, wherein said reverse transcription results in generating at least one cDNA molecule.

21. The method of claim 20, wherein said reverse transcribing step is primed by at least one random primer.

22. The method of claim 20, wherein said reverse transcribing step is primed by a primer attached to said first complementary nucleic acid molecule, said second complementary nucleic acid molecule, or a combination thereof.

23. The method of claim 20, wherein said cDNA molecule comprises at least one promoter sequence.

24. The method of claim 23, wherein said promoter is a bacteriophage transcription promoter.

25. The method of claim 24, wherein said bacteriophage transcription promoter is selected from the group consisting of T7 RNA polymerase promoter, T3 RNA polymerase promoter, SP6 RNA polymerase promoter, and a recombinant promoter.

26. The method of claim 1, wherein said RNA is removed by RNAase digestion.

27. The method of claim 1, wherein said RNA is removed by RNAse digestion, by heating in solution comprising a low concentration of $MgCl_2$, or by a combination thereof.

28. A method to amplify an mRNA molecule, comprising:

obtaining said mRNA molecule;

introducing to said mRNA molecule a first primer, wherein said first primer comprises:

at least two poly(dT)s; and

random sequences;

introducing to said mRNA molecule and said first primer a second primer, wherein said second primer comprises:

at least one riboguanine at the 3′ end of said primer; and

a bacteriophage promoter sequence;

synthesizing a first complementary nucleic acid molecule to said mRNA molecule by extending said first primer using reverse transcriptase under conditions wherein said synthesis results in there being more than one cytosine at the 3′ end of said first complementary nucleic acid molecule, wherein said synthesis results in an mRNA-first complementary nucleic acid molecule hybrid comprising the first primer and its extension product bound to the second primer and the mRNA;

removing said mRNA molecule and said second primer from said hybrid;

synthesizing a second complementary nucleic acid molecule to said first complementary nucleic acid molecule, wherein said synthesis results in a first complementary nucleic acid molecule and second complementary nucleic acid molecule hybrid, wherein the hybrid further comprises both a third primer with a sequence substantially similar to the second primer and an extension product of the third primer bound to the first complementary nucleic acid molecule; and

transcribing at least one mRNA molecule from said first complementary nucleic acid molecule and second complementary nucleic acid molecule hybrid.

29. A method to amplify an mRNA molecule, comprising:

obtaining said mRNA molecule;

introducing to said mRNA molecule a first primer, wherein said first primer comprises:

at least two poly(dT)s; and

a bacteriophage promoter sequence;

introducing to said mRNA molecule and said first primer a second primer, wherein said second primer comprises at least one riboguanine at the 3′ end of said primer;

synthesizing a first complementary nucleic acid molecule to said mRNA molecule by extending said first primer using reverse transcriptase under conditions wherein said synthesis results in there being more than one cytosine at the 3′ end of said first complementary nucleic acid molecule, wherein said synthesis results in an mRNA-first complementary nucleic acid molecule hybrid comprising the first primer and its extension product bound to the second primer and the mRNA;

removing said mRNA molecule and said second primer from said hybrid;

introducing to said complementary nucleic acid molecule an oligo (dNTP) primer with substantially the same sequence as said second primer;

synthesizing a second complementary nucleic acid molecule to said first complementary nucleic acid molecule, wherein said synthesis results in a first complementary nucleic acid molecule and second complementary nucleic acid molecule hybrid; and

transcribing at least one mRNA molecule from said first complementary nucleic acid molecule and second complementary nucleic acid molecule hybrid, wherein said at least one mRNA molecule is an antisense mRNA.

30. A method to amplify an mRNA molecule, comprising:

obtaining said mRNA molecule;

introducing to said mRNA molecule a first primer, wherein said first primer comprises at least two poly(dT)s or a short primer of random sequence;

introducing to said mRNA molecule and said first primer a second primer, wherein said second primer comprises:

at least one riboguanine at the 3′ end of said primer; and

a bacteriophage promoter sequence;

synthesizing a first complementary nucleic acid molecule to said mRNA molecule by extending said first primer using reverse transcriptase under conditions wherein said synthesis results in there being more than one cytosine at the 3′ end of said first complementary nucleic acid molecule, wherein said synthesis results in an mRNA-first complementary nucleic acid molecule hybrid comprising the first primer and its extension product bound to the second primer and the mRNA;

removing said mRNA molecule and said second primer from said hybrid;

introducing to said complementary nucleic acid molecule an oligo (dNTP) primer with substantially the same sequence as said second primer;

synthesizing a second complementary nucleic acid molecule to said first complementary nucleic acid molecule, wherein said synthesis results in a first complementary nucleic acid molecule and second complementary nucleic acid molecule hybrid; and

transcribing at least one mRNA molecule from said first complementary nucleic acid molecule and second complementary nucleic acid molecule hybrid, wherein said at least one mRNA molecule is a sense mRNA molecule.

31. A kit for amplifying an RNA molecule using the method of claim 1, wherein said kit is in a suitable container and comprises said first primer, said second primer, said third primer, or a combination thereof.

32. The kit of claim 31, wherein said first primer is a short primer of random sequences.

33. The kit of claim 31, wherein said first primer further comprises a region selected from the group consisting of a promoter, a restriction enzyme digestion sequence, and a combination thereof.

34. The kit of claim 31, wherein said second primer further comprises a region selected from the group consisting of a promoter, a restriction enzyme digestion sequence, and a combination thereof.

35. A method of providing a substrate for *in vitro* transcription, comprising:

obtaining said mRNA molecule;

introducing to said mRNA molecule a first primer, wherein said first primer comprises a region which anneals under suitable conditions to a complementary region of said mRNA molecule;

introducing to said mRNA molecule and said first primer a second primer, wherein said second primer comprises at least one riboguanine at the 3′ end of said primer;

synthesizing a first complementary nucleic acid molecule to said mRNA molecule by extending said first primer using reverse transcriptase under conditions wherein said synthesis results in there being more than one cytosine at the 3′ end of said first complementary nucleic acid molecule, wherein said synthesis results in an mRNA-first complementary nucleic acid molecule hybrid comprising the first primer and its extension product bound to the second primer and the mRNA;

removing said mRNA molecule and said second primer from said hybrid;

synthesizing a second complementary nucleic acid molecule to said first complementary nucleic acid molecule, wherein said synthesis results in a first complementary nucleic acid molecule and second complementary nucleic acid molecule hybrid, wherein the hybrid further comprises both a third primer with a sequence substantially similar to the second primer and an extension product of the third primer bound to the first complementary nucleic acid molecule; and

transcribing at least one mRNA molecule from said first complementary nucleic acid molecule and second complementary nucleic acid molecule hybrid.

36. A method of detecting an RNA from a histologically-stained cell, comprising:
obtaining the cell;
extracting RNA from the cell; and
amplifying the RNA.

37. The method of claim 36, wherein the cell is in a tissue.

38. A method of detecting an RNA from a cell, comprising:
obtaining the cell;
histologically staining the cell;
extracting RNA from the cell; and
amplifying the RNA.

39. The method of claim 38, wherein the cell is in a tissue.

40. The method of claim 39, wherein the tissue is fresh tissue.

41. The method of claim 39, wherein the tissue is fixed tissue.

42. The method of claim 41, wherein the tissue is fixed by acetone, aldehyde derivatives, ethanol, or combinations thereof.

43. The method of claim 36 or 38, wherein said cell is from a physiological body fluid, a pathological exudate, or a pathological transudate.

44. The method of claim 43, wherein the physiological body fluid is blood, cerebrospinal fluid, urine, sweat, semen, or saliva.

45. The method of claim 38, wherein the cells are in blood, bone marrow, cerebrospinal fluid, or any other physiological body fluids or any pathological exudates or transudates.

46. The method of claim 36 or 38, wherein said cell is from bone marrow.

47. The method of claim 36 or 38, wherein said cell is from *in vitro* cultured cells.

48. The method of claim 36 or 38, wherein the histological stain identifies cellular structures.

49. The method of claim 48, wherein said cellular structures are mitochondria, centrioles, rough endoplasmic reticulum, smooth endoplasmic reticulum, peroxisomes, endosomes, lysosomes, vesicles, Golgi apparatus, nucleus, cytoplasm, or a combination thereof.

50. The method of claim 37 or 39, wherein the histological stain identifies tissue structures.

51. The method of claim 50, wherein said tissue structures are structures of lamina, matrix, or a combination thereof.

52. The method of claim 36 or 38, wherein the histological stain is Acid black 1, Acid blue 22, Acid blue 93, Acid fuchsin, Acid green, Acid green 1, Acid green 5, Acid magenta, Acid orange 10, Acid red 26, Acid red 29, Acid red 44, Acid red 51, Acid red 66, Acid red 87, Acid red 91, Acid red 92, Acid red 94, Acid red 101, Acid red 103, Acid roseine, Acid rubin, Acid violet 19, Acid yellow 1, Acid yellow 9, Acid yellow 23, Acid yellow 24, Acid yellow 36, Acid yellow 73, Acid yellow S, Acridine orange, Acriflavine, Alcian blue, Alcian yellow, Alcohol soluble eosin, Alizarin, Alizarin blue 2RC, Alizarin carmine, Alizarin cyanin BBS, Alizarol cyanin R, Alizarin red S, Alizarin purpurin, Aluminon, Amido black 10B, Amidoschwarz, Aniline blue WS, Anthracene blue SWR, Auramine O, Azocarmine B, Azocarmine G, Azoic diazo 5, Azoic diazo 48, Azure A, Azure B, Azure C, Basic blue 8, Basic blue 9, Basic blue 12, Basic blue 15, Basic blue 17, Basic blue 20, Basic blue 26, Basic brown 1, Basic fuchsin, Basic green 4, Basic orange 14, Basic red 2, Basic red 5, Basic red 9, Basic violet 2, Basic violet 3, Basic violet 4, Basic violet 10,

Basic violet 14, Basic yellow 1, Basic yellow 2, Biebrich scarlet, Bismarck brown Y, Brilliant crystal scarlet 6R, Calcium red, Carmine, Carminic acid, Celestine blue B, China blue, Cochineal, Coelestine blue, Chrome violet CG, Chromotrope 2R, Chromoxane cyanin R, Congo corinth, Congo red, Cotton blue, Cotton red, Croceine scarlet, Crocin, Crystal ponceau 6R, Crystal violet, Dahlia, Diamond green B, Direct blue 14, Direct blue 58, Direct red, Direct red 10, Direct red 28, Direct red 80, Direct yellow 7, Eosin B, Eosin Bluish, Eosin, Eosin Y, Eosin yellowish, Eosinol, Erie garnet B, Eriochrome cyanin R, Erythrosin B, Ethyl eosin, Ethyl green, Ethyl violet, Evans blue, Fast blue B, Fast green FCF, Fast red B, Fast yellow, Fluorescein, Food green 3, Gallein, Gallamine blue, Gallocyanin, Gentian violet, Haematein, Haematine, Haematoxylin, Helio fast rubin BBL, Helvetia blue, Hematein, Hematine, Hematoxylin, Hoffman's violet, Imperial red, Ingrain blue, Ingrain blue 1, Ingrain yellow 1, INT, Kermes, Kermesic acid, Kernechtrot, Lac, Laccaic acid, Lauth's violet, Light green, Lissamine green SF, Luxol fast blue, Magenta 0, Magenta I, Magenta II, Magenta III, Malachite green, Manchester brown, Martius yellow, Merbromin, Mercurochrome, Metanil yellow, Methylene azure A, Methylene azure B, Methylene azure C, Methylene blue, Methyl blue, Methyl green, Methyl violet, Methyl violet 2B, Methyl violet 10B, Mordant blue 3, Mordant blue 10, Mordant blue 14, Mordant blue 23, Mordant blue 32, Mordant blue 45, Mordant red 3, Mordant red 11, Mordant violet 25, Mordant violet 39 Naphthol blue black, Naphthol green B, Naphthol yellow S, Natural black 1, Natural red, Natural red 3, Natural red 4, Natural red 8, Natural red 16, Natural red 25, Natural red 28, Natural yellow 6, NBT, Neutral red, New fuchsin, Niagara blue 3B, Night blue, Nile blue, Nile blue A, Nile blue oxazone, Nile blue sulphate, Nile red, Nitro BT, Nitro blue tetrazolium, Nuclear fast red, Oil red O, Orange G, Orcein, Pararosanilin, Phloxine B, Picric acid, Ponceau 2R, Ponceau 6R, Ponceau B, Ponceau de Xylidine, Ponceau S, Primula, Purpurin, Pyronin B, Pyronin G, Pyronin Y, Rhodamine B, Rosanilin, Rose bengal, Saffron, Safranin O, Scarlet R, Scarlet red, Scharlach R, Shellac, Sirius red F3B, Solochrome cyanin R, Soluble blue, Solvent black 3, Solvent blue 38, Solvent red 23, Solvent red 24, Solvent red 27, Solvent red 45, Solvent yellow 94, Spirit soluble eosin, Sudan III, Sudan IV, Sudan black B, Sulfur yellow S, Swiss blue, Tartrazine, Thioflavine S, Thioflavine T, Thionin, Toluidine blue, Toluyline red, Tropaeolin G, Trypaflavine, Trypan blue, Uranin, Victoria blue 4R, Victoria blue B, Victoria green B, Water blue I, Water soluble eosin, Xylidine ponceau, or Yellowish eosin.

53. The method of claim 37 or 39, wherein the extracting step further comprises dissection of the cell from the tissue.

54. The method of claim 53, wherein the dissection is from a micropipette on a micromanipulator or by laser capture microdissection.

55. The method of claim 36, wherein the amplifying step further comprises synthesis of cDNA from the RNA.

56. The method of claim 55, wherein the synthesis of cDNA further comprises synthesizing the cDNA by reverse transcriptase with an oligonucleotide that binds the RNA.

57. The method of claim 36, wherein the RNA amplification method is *in vitro* transcription.

58. The method of claim 36, wherein the amplification is by a method which comprises:

introducing to said RNA molecule a first primer, wherein said first primer comprises a region that hybridizes under suitable conditions to a complementary region of said RNA molecule;

introducing to said RNA molecule and said first primer a second primer, wherein said second primer comprises at least one riboguanine at the 3′ end of said primer;

synthesizing a first complementary nucleic acid molecule to said RNA molecule by extending said first primer using reverse transcriptase under conditions wherein said synthesis results in there being more than one cytosine at the 3′ end of said first complementary nucleic acid molecule, wherein said synthesis results in an RNA-first complementary nucleic acid molecule hybrid comprising the first primer and its extension product bound to the second primer and the RNA;

removing said RNA molecule and said second primer from said hybrid;

synthesizing a second complementary nucleic acid molecule to said first complementary nucleic acid molecule, wherein said synthesis results in a first complementary nucleic acid molecule and second complementary nucleic acid molecule hybrid, wherein the hybrid further comprises both a third primer with a sequence substantially similar to the second primer and an extension product of the third primer bound to the first complementary nucleic acid molecule; and

transcribing at least one mRNA molecule from said first complementary nucleic acid molecule and second complementary nucleic acid molecule hybrid.

59. A kit, housed in a suitable container, for the detection of RNA from a cell in a histologically-stained tissue, comprising dye/histological stain, RNA extraction reagent, RNA precipitation carrier, oligo (dT) primer, reverse transcriptase, DNA polymerase, RNA

polymerase, RNAse inactivating agent, terminal continuation oligonucleotide, dNTPs, NTPs, or a combination thereof.

60. The kit of claim 59, wherein the RNA polymerase is T7 RNA polymerase, T3 RNA polymerase, or SP6 RNA polymerase.

61. The kit of claim 59, wherein the kit further comprises a vector, a ligase, or a combination thereof.

62. The kit of claim 59, wherein the dye/histological stain is Acid black 1, Acid blue 22, Acid blue 93, Acid fuchsin, Acid green, Acid green 1, Acid green 5, Acid magenta, Acid orange 10, Acid red 26, Acid red 29, Acid red 44, Acid red 51, Acid red 66, Acid red 87, Acid red 91, Acid red 92, Acid red 94, Acid red 101, Acid red 103, Acid roseine, Acid rubin, Acid violet 19, Acid yellow 1, Acid yellow 9, Acid yellow 23, Acid yellow 24, Acid yellow 36, Acid yellow 73, Acid yellow S, Acridine orange, Acriflavine, Alcian blue, Alcian yellow, Alcohol soluble eosin, Alizarin, Alizarin blue 2RC, Alizarin carmine, Alizarin cyanin BBS, Alizarol cyanin R, Alizarin red S, Alizarin purpurin, Aluminon, Amido black 10B, Amidoschwarz, Aniline blue WS, Anthracene blue SWR, Auramine O, Azocarmine B, Azocarmine G, Azoic diazo 5, Azoic diazo 48, Azure A, Azure B, Azure C, Basic blue 8, Basic blue 9, Basic blue 12, Basic blue 15, Basic blue 17, Basic blue 20, Basic blue 26, Basic brown 1, Basic fuchsin, Basic green 4, Basic orange 14, Basic red 2, Basic red 5, Basic red 9, Basic violet 2, Basic violet 3, Basic violet 4, Basic violet 10, Basic violet 14, Basic yellow 1, Basic yellow 2, Biebrich scarlet, Bismarck brown Y, Brilliant crystal scarlet 6R, Calcium red, Carmine, Carminic acid, Celestine blue B, China blue, Cochineal, Coelestine blue, Chrome violet CG, Chromotrope 2R, Chromoxane cyanin R, Congo corinth, Congo red, Cotton blue, Cotton red, Croceine scarlet, Crocin, Crystal ponceau 6R, Crystal violet, Dahlia, Diamond green B, Direct blue 14, Direct blue 58, Direct red, Direct red 10, Direct red 28, Direct red 80, Direct yellow 7, Eosin B, Eosin Bluish, Eosin, Eosin Y, Eosin yellowish, Eosinol, Erie garnet B, Eriochrome cyanin R, Erythrosin B, Ethyl eosin, Ethyl green, Ethyl violet, Evans blue, Fast blue B, Fast green FCF, Fast red B, Fast yellow, Fluorescein, Food green 3, Gallein, Gallamine blue, Gallocyanin, Gentian violet, Haematein, Haematine, Haematoxylin, Helio fast rubin BBL, Helvetia blue, Hematein, Hematine, Hematoxylin, Hoffman's violet, Imperial red, Ingrain blue, Ingrain blue 1, Ingrain yellow 1, INT, Kermes, Kermesic acid, Kernechtrot, Lac, Laccaic acid, Lauth's violet, Light green, Lissamine green SF, Luxol fast blue, Magenta 0, Magenta I, Magenta II, Magenta III, Malachite green, Manchester brown, Martius yellow, Merbromin, Mercurochrome, Metanil yellow, Methylene azure A, Methylene azure B, Methylene azure C, Methylene blue, Methyl blue, Methyl green, Methyl violet,

Methyl violet 2B, Methyl violet 10B, Mordant blue 3, Mordant blue 10, Mordant blue 14, Mordant blue 23, Mordant blue 32, Mordant blue 45, Mordant red 3, Mordant red 11, Mordant violet 25, Mordant violet 39 Naphthol blue black, Naphthol green B, Naphthol yellow S, Natural black 1, Natural red, Natural red 3, Natural red 4, Natural red 8, Natural red 16, Natural red 25, Natural red 28, Natural yellow 6, NBT, Neutral red, New fuchsin, Niagara blue 3B, Night blue, Nile blue, Nile blue A, Nile blue oxazone, Nile blue sulfate, Nile red, Nitro BT, Nitro blue tetrazolium, Nuclear fast red, Oil red O, Orange G, Orcein, Pararosanilin, Phloxine B, Picric acid, Ponceau 2R, Ponceau 6R, Ponceau B, Ponceau de Xylidine, Ponceau S, Primula, Purpurin, Pyronin B, Pyronin G, Pyronin Y, Rhodamine B, Rosanilin, Rose bengal, Saffron, Safranin O, Scarlet R, Scarlet red, Scharlach R, Shellac, Sirius red F3B, Solochrome cyanin R, Soluble blue, Solvent black 3, Solvent blue 38, Solvent red 23, Solvent red 24, Solvent red 27, Solvent red 45, Solvent yellow 94, Spirit soluble eosin, Sudan III, Sudan IV, Sudan black B, Sulfur yellow S, Swiss blue, Tartrazine, Thioflavine S, Thioflavine T, Thionin, Toluidine blue, Toluyline red, Tropaeolin G, Trypaflavine, Trypan blue, Uranin, Victoria blue 4R, Victoria blue B, Victoria green B, Water blue I, Water soluble eosin, Xylidine ponceau, or Yellowish eosin.

63. A method of incorporating a nucleic acid sequence to a 3′ region of a synthesized nucleic acid strand comprising:

incubating a target nucleic acid strand with a terminal continuation oligonucleotide, and a first strand synthesis primer which is complementary to a region at the 3′ end or a region upstream of the 3′ end of the target nucleic acid strand under conditions that facilitate hybridization of the first strand synthesis primer to the target nucleic acid strand; and

extending the primer, wherein the extending is carried out with a polymerase such that extension synthesizes a nucleic acid strand comprising the first strand synthesis primer, a complementary sequence of the target nucleic acid strand, and a complement of the terminal continuation oligonucleotide.

64. The method of claim 63 wherein the terminal continuation oligonucleotide contains at least one guanine, deoxyguanine, cytosine, or deoxycytosine at the 3′ end of the terminal continuation oligonucleotide.

65. The method of claim 63 wherein the target nucleic acid strand is RNA and the polymerase is reverse-transcriptase, such that the nucleic acid synthesized in the extending step is a first strand cDNA comprising the first strand synthesis primer, a complement of the

target nucleic acid strand, and a complement of the terminal continuation oligonucleotide at the 3′ end.

66. The method of claim 65 wherein the RNA is mRNA.

67. The method of claim 65 wherein the first strand synthesis primer comprises at least two thymidine residues at its 3′ end.

68. The method of claim 65 wherein the first strand synthesis primer comprises a random hexamer sequence of nucleic acid.

69. The method of claim 65 wherein the terminal continuation oligonucleotide comprises at least two nucleotides selected from a group consisting of guanine, deoxyguanine, cytosine or deoxycytosine bases.

70. The method of claim 65 comprising the additional steps:

incubating the first strand cDNA with the terminal continuation oligonucleotide under conditions that facilitate hybridization of the terminal continuation oligonucleotide to the first strand cDNA; and

extending the terminal continuation oligonucleotide, wherein said extending is carried out with a DNA polymerase such that extension synthesizes a second strand cDNA comprising the sequence of the terminal continuation oligonucleotide and a complementary sequence of the first strand cDNA.

71. The method of claim 70 wherein the DNA polymerase is *Taq* polymerase.

72. The method of claim 70 wherein the first strand synthesis primer comprises a transcriptional promoter sequence.

73. The method of claim 70 wherein the terminal continuation oligonucleotide comprises a transcriptional promoter sequence and at least one guanine, deoxyguanine, cytosine, or deoxycytosine at the 3′ end of the terminal continuation oligonucleotide.

74. The method of claim 70, wherein the terminal continuation oligonucleotide comprises a transcriptional promoter sequence and at least one guanine or cytosine at the 3′ end of the terminal continuation oligonucleotide.

75. The method of claim 74 comprising the additional steps:

incubating the second strand cDNA with a RNA polymerase capable of binding to the transcriptional promoter sequence; and

transcribing the second strand cDNA wherein the transcribing synthesizes a RNA transcript complementary in sequence to the second strand cDNA.

76. The method of claim 73 comprising the additional steps:

incubating the first strand cDNA with a RNA polymerase capable of binding to the transcriptional promoter sequence; and

transcribing the first strand cDNA wherein the transcribing synthesizes a RNA transcript complementary in sequence to the first strand cDNA.

77. The method of claim 70 wherein the first strand synthesis primer comprises a transcriptional promoter sequence and wherein the terminal continuation oligonucleotide comprises at least one guanine, deoxyguanine, cytosine, or deoxycytosine at its 3′ end and a transcriptional promoter sequence different from the transcriptional promoter sequence in the first strand synthesis primer.

78. The method of claim 77 comprising the additional steps:

incubating the first strand cDNA with a RNA polymerase capable of binding to the transcriptional promoter sequence located on the first strand cDNA;

transcribing the first strand cDNA wherein the transcribing synthesizes a RNA transcript complementary in sequence to the first strand cDNA;

incubating the second cDNA strand with a RNA polymerase capable of binding to the transcriptional promoter sequence located on the second strand cDNA; and

transcribing the second strand cDNA wherein the transcribing synthesizes a RNA transcript complementary in sequence to the second strand cDNA.

79. The method of claim 75 or 78 wherein the synthesized RNA transcripts are used as templates for *in vitro* translation.